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AR153576 3715 bp DNA
Sequence 10 from patent US 6235872.
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HUMARC1 AF321915 AF321917

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HSARP

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AL049564 Human DNA M34233 Human andro M73069 Human andro U94177 Pan troglod AF162704 Homo sapi U94179 Macaca fasc

M23263 Human andro 109479 Sequence 1 109510 Sequence 1 M20132 Human andro

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Description

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08-AUG-2001

PAT

GI:15121108

ALIGNMENTS

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

source

BASE COUNT ORIGIN

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1 2079 TT	3486 g 2139 G	3546 g. 1 2199 G.	3606 a 1 2259 A	3666 c 2319 C	3726 g 1 2379 G	3786 g. 2439 G.	3846 g	3906 gi 2559 Gi	3966 to 2619 To	4026 g	4086 to 2739 TO	4146 ca 2799 C	4206 gtc 111 2859 GTC	4266 cc 	4326 ag 2979 AG	4386 ac 11 3039 AC	4446 cc 3099 CC	4506 tt
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raft entry and computer-readable sequence for [1] kindly provided 7 S.Liao, 01-MAR-1989.

Variation of different sizes were found. These proteins could be explained if alternative start codons at positions 1084, 1252 and 1315 were used. ukaryott, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; anmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. (bases I to 3115, J. and Liao, S.T. tructural analysis of complementary DNA and amino acid sequences f human and rat androgen receptors occ. Matl. Acad. Sci. U.S.A. 85 (19), 7211-7215 (1988) catctctgtgcaagtgcccaagatctttctgggaaagtcaagcccatctatttcca 4625 GACCTGCTAATCAAGTCACACATGGTGAGCGTGGACTTTCCGGAAATGATGGCAGA 3218 ocacaaacytttacttatcttatgccacyggaaytttagagagctaagattatctgg 5045 (sites)
hang, C.S., Kokontis, J. and Liao, S.T.
blecular cloning of human and rat complementary DNA encoding 31-OCT-1994 cctgcctgttataactctgcactactcctgcagtgccttggggaatttcctctat Human androgen receptor mRNA, complete cds.
M23263 N18624
M23263.1 G1:178893
Indrogen receptor; dihydrotestosterone receptor.
Omo saplens
ikarotes... 1. .3715 /organism="Homo sapiens" /db_xref="taxon:9606" /map="Xq11.2-q12" 532. .3288 drogen receptors Hence 240 (4850), 324-326 (1988) H78111 Location/Qualifiers aatcaaaacaaaa 5062

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Z q	2979	agydyalgydcigaaaaalcaaaaattettigatgaacttigaatgaatgaetaaatsaagga 	4385 3038
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P G	3339	LCTTCTGCCTGTTATAACTCTGCACTACTCCTCTGCAGTGCCTTGGGGGATTTCCTCTAT . 	4745 3398
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LOCU: DEFII	S NITION SSION	109479 3721 bp PAT 02-DEC-196 Sequence 1 from Patent WO 8909223. 109479	94
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( pases 1 to 3721)
Liao,S. and Chang,C-S.
DNA BINDING PROTEINS INCLUDING ANDROGEN 1
Patent: WO 8909223-A 1 05-OCT-1989;
Location/Qualifiers
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432, 297 438 303 444	Db 3099 CTTCTACCAGCTCACCAAGCTCCTGG Qy 4500 gttcacttttgacctgctaatcaag1	3219 4620 3279 4680	3339 C 4740 C 3399 C	3448 3448 4860 3508	Oy 4920 aatcegagacgatccacatcaggco	RESULT 4 109510 3569 bp 109510 3569 bp 109510 3569 bp 360510N 3604000 3609 bp 360510N 360510 360782 3600000 36000000 3600000000000000	REFERENCE 1 (bases 1 to 3569) AUTHORS French, F.S., Wilson, E.D. TITLE DNA ENCODING ANDROGEN FOURNAL PATENT: WO 8909791-A 1 FEATURES 1.3569 BASE COUNT 796 a 1009 c 9001GIN
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qq	3039	SGAACTCGATCGTATCATTG
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Qy	4500	55
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Qy	4560	
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Οy	4680	agatgtettetgeetgttataaetetgeaetaeteeteetgeagtgeettggggaattte 473
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 Dp	3399	rgatgtacagtctgtcatgGaattctatttgctggcT
Qγ	4800	tttetetttetetetettetttettettettectecetatetaaceteceatggeacet 4859
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Qy	4860	gactttgcttcccattgtggctcctatctgtgttttgaatggtgttgtatgccttt
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Qy	4920	497
qu	3568	AICIGIGAIGAICCTCATAIGGCCCAGIGTCAAGITGTGTTTTACAGCACTACTC
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 qq	3628	SCCAGCCACACAAACGTTTACTTATCTTATGCCACGGCAAGTTTAGAGAGCTAAGAT
Qy	5040	atctggggaaatcaaaacaaaaa 5062
Db	3688	ATCTGGGGAAATCAAAAAA 3710
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LOCUS	US	109510 3569 bp PAT 02-DEC-1994 N Sequence 1 from Patent WO 8909791.
ACC	ACCESSION VERSION	
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 REFER	ENC	Unclassified. [(bases 1 to 3569)
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1922 gaagagetttccagaatctgttccagagetgegeagtgatccagaaccagggcccca 421 GAGGAGCTTCCAGAATCGTCCAGAACCCGGGCCCCA 48 421 GAGGAGCTTCCAGAATCGTTCCAGAACCCGGCGCCCCA 48 481 GAGGAGCTTCCAGAATCGTTCCAGAACCCGGCGCCCCA 48 481 GAGGAGCTTCCAGAATCGTCCCGCGCCCCAGACCCGCGCCCCAGACCCGCGCCCCGCTTTGCTGCTGCTGCTCTCCTGCTGCTCTCCTGCTG	QY	862 ggatggaagtgcagttagggctgggaaggtctacctcggccgccgtccaagacctacc 19
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Draft entry and computer readable sequence [1] kindly submitted by E.M.Wilson, 18 AUG-1988.
Location/Qualifiers
1. 3569
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Lubahn,D.B., Joseph,D.R., Sar,M., Tan,J., Higgs,H.N., Larson,R.E.
Erench,F.S. and Wilson,E.M.
The human androgen receptor: complementary deoxyribonucleic acid
cloning, sequence analysis and gene expression in prostate
Mol. Endocrinol. 2 (12), 1265-1275 (1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                              4802 tetetttetetetettttttttttettetteeteeetatetaaeceteeeatggeaeette
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      HUMANDREC 3569 bp mRNA PRI Human androgen receptor (AR) mRNA, complete cds. M20132 J03180 M20132.1 GI:178627
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2521 2701 1188 2761 1248 2821 2941 1428 1488 2461 2881 3001 1548 3121 1608 3301 3061 1668 3241 1848 1908 1968 948 3181 3361 3421 3481 3541 ccacttcctccaaggacaattacttagggggcacttcgaccatttctgacaacgccaagg gcgcaggcaagagcactgaagatactgctgagtattcccctttcaagggaggttacacca cgccgcctccccatcccacgctcgcatcaagctggagaacccgctggactacggcagcg acatgogtttggagactgccagggaccatgttttgcccattgactattactttccaccc ctgtagccccctacggctacactcggcccctcagggggctggcgggccaggaaagcgact tcaccgcacctgatgtgtggtaccctggcggcatggtgagcagagtgccctatcccagtc ccgctgaccttaaagacatcctgagcgaggccagcacca 949 1009 1069 2402 889 2462 2522 2582 2642 1129 2702 1189 2762 1249 2822 1309 2882 1369 2942 1429 3002 1489 3062 1549 1609 1729 3122 3182 1669 3242 3302 3362 1849 1789 3422 3482 Q 90 δ g QΫ q QV Db Db qq qq QΛ ÓΥ QQ Ω Qγ Qy Db Qγ q Qγ ΩD Qγ QQ Ωy qq QQ qq Qγ QY Qγ qq qq δŻ Ω QQ δ

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2028 8601 2088 8661	2148 3721 2208	3781 2268	3841	3901 2388	3961 2448	4021 2508	4081	4141	4201 2688	4261 2748	4321	4381	4441	4501 2988	4561 3048	4621
		3722 ttcggaaatgttatgaagcagggatgactctgggagcccggaagctgaagaacttggta 3 	3782 atctgaaactacaggaggaggaggaggctccagcaccaccagccccactgaggagacaa 3	3842 cccagaagctgacagtytcacacattyaaggctatgaatgtcagcccatctttctgaatg 3	3902 tcctggaagccattgagccaggtgtagtgtgtgtgtgacacagacaaccagcccgact 3	3962 cctttgcagccttgctctctagcctcaatgaactgggagagaga	4022 tcaagtgggccaaggccttgcctggcttccgcaacttacacgtggacgaccagatggctg 4	4082 tcattcagtactcctggatggggctcatggtgtttgccatgggctggcgatccttcacca 4	4142 atgtcaactccaggatgctctacttcgcccctgatctggtttcaatgagtaccgcatgc 4	4202 acaagtcccggatgtacagccagtgtgtccgaatgagcacctctctcaagagtttggat 4	4262 ggctccaaatcacccccaggaattcctgtgcatgaaagcactgctactcttcagcatta (4322 ttccagtggatgggctgaaaaatcaaaaattctttgatgaacttcgaatgaactacatca (4382 aggaactcgatcgtatcattgcatgcaaaagaaaaaatcccacatcctgctcaagacgct	4442 tctaccagctcaccaagctcctggactccgtgcagcctattgcgagagagctgcatcagt	4502 tcacttttgacctgctaatcaagtcacacatggtgagcgtggactttccggaaatgatgg 	4562 cagagatcatctctgtgcaagtgcccaagatcctttctgggaaagtcaagcccatctatt
oy Oy Oy	90 VO PD	QY	Qy Db	QY	Oy Db	ογ Db	Qy	Qy	Qy Dp	QY	QY Dp	QY	Qy	Qy Db	Oy Db	Qy

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AL (Dayles) In Colored to Control, Hinxton, Cambridgeshire, Direct Submission

Also May 27, 1999 this sequence version replaced gi:4757056.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known submissions.
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Em:, EMBL, Sw., SWISSPROT; Tr., TREMBL, Wp:, WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSDJ80804 139033 bp DNA PRI 14-APR-2000 Human DNA sequence from clone RP4-80804 on chromosome Xq11.1-12. Contains the 5' end of the AR gene for androgen receptor (dihydrotestosterone receptor), a PABPN1 (poly(A)-binding protein, nuclear 1) (PABP2) pseudogene, ESTS STSS, GSSS and two putative CpG AL049564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 139033)
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                                                                                                                                                                                                                                                                                                                                            4861
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4922 tetgtgatgatecteatatggeeeagtgteaagttgtgettgtttaeageaetaetetgt 4981
3049 CAGAGATCATCTCTGTGCCAAGTGCCCAAGATCCTTTCTGGGAAAGTCAAGCCCATCTATT 3108
                                                                                                                                            4742 ctattgatgtacagtctgtcatgaacatgttcctgaattctatttgctgggcttttttt
                                                                                                                                                                                                                                                                  3289 TCTCTTCTCTCTTTTTTTTTTTTTTTCCCCCCTATCTAACCCTCCCATGGCACCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                           4862 agactttgcttcccattgtggctcctatctgtgttttgaatggtgttgtatgcctttaaa
                                                                                                                                                                                                                                                                                                                                               4802 tetetttetetetettetttettetteeteeteeetatetaaceeteeeatggeaeette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gecagecacacaaacgtttacttatettatgecacgggaagtttagagagetaagattat
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TITLE
JOURNAL
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SOURCE
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.6171 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         //orde="match: cDNAs: Em:856585 Em:U94176 Em:M23264 Em:U94178 Em:U94179 Em:AF197950 Em:X59592 Em:M20133 Em:AF162704 Em:X53779 Em:M34233 Em:U94177 Em:M23263 Em:M73069 Em:L29496 Em:M20132 Em:M21748"
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35467. .36249
/note="CpG island"
45627. .35758
/note="66 copies 2 mer gg 65% conserved"
38519. .38694
/note="L2 repeat: matches 1960. .2143 of consensus"
38707. .39983
                                                  repeat: matches 1. .257 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33451. 33896
/note="CpG island"
/evidence=not_experimental
33516. 33595
/note="40 copies 2 mer cc 67% conserved"
33256. 33597
/note="24 copies 3 mer cgc 90% conserved"
/gene="24 copies 3 mer cgc 90% conserved"
/gene="24 copies 3 mer cgc 90% conserved"
                                                                                                                                                                                                                  /note="10" copies 2 mer ag 80% conserved" 29068. 29089. /note="11" copies 2 mer aa 100% conserved" 29409. 29440
                                                                                                                                                                                                                                                                                                                                      /note="16 copies 2 mer tt 87% conserved" 30933. .31064
/note="2 copies 66 mer 91% conserved" complement(<33330. .35469)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="37 copies 3 mer ctg 86% conserved"
complement(34943, .35357)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /evidence=not_experimental
/product="6J80804.1 (androgen receptor
(dihydrotestosterone receptor))"
complement(33330. .35469)
/gene="AR"
                                                                        /note="LIMB8 repeat: matches 4282.
28780. .29241
                                                                                                                                                                      Em: AQ729644"
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/note="match: STS: Em:M58158"
35302. .35355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(<33330. .34945)
                                                                                                                                                         /note="match: GSS:
28936. .28975
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="AR"
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                                                                                                                                          This sequence is the entire insert of clone RP4-80804 The true left end of clone RP6-22P16 is at 91045 in this sequence. This sequence was generated from part of bacterial clone contigs of human chromosome X, constructed by the Sanger Centre Chromosome X Bapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chrx.
http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP4-80804 is
from the library RPCI-4 constructed at the Roswell Park Cancer
Institute by the group of Pieter de Jong. For further details see
http://bacpac.med.buffalo.edu/
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//note="WIR repeat: matches 55. .214 of consensus"

15460. 15631

//note="Will repeat: matches 3299. .3469 of consensus"

16596. 16852
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/note="MIR repeat: matches 48. .121 of consensus" .22607. .23595
/note="L2 repeat: matches 1750. .2747 of consensus" 23800. .23933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="MIR repeat: matches 22. .154 of consensus" 24989. .25151
/note="L2 repeat: matches 2596. .2744 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .166 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .279 of consensus"
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17829. 18163
Anote-"Alusg repeat: matches 1. .310 of consensus"
18439. .18638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anote="MIR repeat: matches 20. .262 of consensus" 1392. .1589
Anote="MIR repeat: matches 19. .243 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3309. .6415
Mote="MIR repeat: matches 65. .176 of consensus"
020. .7160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="MIR repeat: matches 48. .188 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      // note="WIR repeat: matches 53. .247 of consensus" 13762. .13886 // note="12 repeat: matches 2572. .2705 of consensus" 13939. .14173 // note="match: STS: Em:AF020219" // 14100. .14370 // note="match: Repeat: matches 1. .279 of consensus" // note="matches 1. .279 of consensus" // note="matc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .149 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="MIR repeat: matches 34. .139 of consensus" 7681. .17742
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="MIR repeat: matches 4. .262 of consensus"
21954. .22035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .227 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .262 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9322. 9414
/note="3 copies 31 mer 82% conserved"
9828. 9949
/note="61 copies 2 mer ac 59% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         227. 3172
note="LIMB8 repeat: matches 5259.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1041. .8086
note="MIR repeat: matches 118.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12334. .12460

Mote="MIR repeat: matches 20.

13084. .13274
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21624. .21836
                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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933. .1165
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matches 4835.
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                L2 repeat: matches 2130.
.40809
                                                        /note="L2 repeat: matches 1990.
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complement(41397. 41704)
                                                                               .....ur(41397. .41704)
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note="ma*r-"
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                                                                                                                                                                                   Score 3185.4;
Pred. No. 0;
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                                                                                                                                                                                    62.78;
97.78;
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                             40676.
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Matches 3428; Conserv
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35267 35506 CAGCACTGCACGACCCGCCTGGTTAGGCTGCACGCGGAGAACCCTCTGTTTTCC 35447 1302 GCA - - AACTGTTGCATTTGCTCTCCCACCTCCCCCCCCTCCGAGATCCCGGGGAGCC 36044 1123 teggeccagegntgneagneegagtttgeagagagtaacteeetttggetgegageggg cagcactgcagccacgaccngcctggttaggctgcacgcggagagaaccctctgttttcc ccgaaataaaagaaaaagataataactcagttcttatttgcacctacttcagtggacact accettcaagtattaagagacagactgtgagcctagcagggcagatcttgtccaccgtgt ACCCTTCAAGTATTAAGAGACAGACTGTGAGCCTAGCAGGGCAGATCTTGTCCACCGTGT agitteettetetagaagetteeegeaggigggeagetagetgeagegactacegeateat cacageetgttgaaetettettgageaagagaaggggaggeggggtaagggaagtaggtgg cccactetetetecaceteeteetgeetteeecaeceegagtgeggageeagagateaaa aggaagcaaggaaagtgcctggtaggactgacggctgcctttgtcctcctctccacc teggetaeteteagecaaececeteaceaecetteteeceaecegeceeeggeeeegg cogectececcaceetgeetteececectececogtettetetecegeagetgeeteag agettgetgggagagegggaacggteeggageaageecagaggeaggaggaggegaeaga 35326 1603 1723 35266 35206 35086 1184 1244 1303 1423 35386 1483 1543 1663 35146 1783 1004 1064 35745 35565 1363 771 36043 831 890 35925 944 35865 35805 1124 35685 35625

Qy 2923 Db 33892	3383	Qy 3043 Db 33772	Qy 3103 Db 33712	Qy 3163 Db 33652	3359	3353.	3347	QY 3403 a	Qy 3463 t	RESULT 7 HUMARX LOCUS	ZOHO	SOURCE ORGANISM	REFERENCE AUTHORS TITLE	JOURNAL MEDLINE FEATURES SOUTCE	dene	CDS	
1843 aagattcagccaagctcaaggatggaagtgcagttagggctgggaaggtctacctcgg 1902 	cagagogtgogogaagtg 196 	1963 atccagaaccgggcccaggcaccagaggcgcgcgagcagcactcccggcgcagt 2022 	2023 ttgctgctgctgcagcagcagcagcagcagcagcagcagcagcagcagcag	2083 cagcagcagcagcagcagcagcaagagactagccccaggcagcagcagcagcagcagcag 2142 	2143 ggtgaggatggttctccccaagcccatcgtagaggccccacaggctacctggtcctggat 2202 	2203 gaggaacagcaaccttcacagccgcagtcggccctggagtgccacccggagaggttgc 2262 	2263 gtcccagagcctggagccgccgtggccgccagcaagggctgccgcagcagcagcagca 2322 	2323 cctccggacgaggatgactcagctgcccatccacgttgtccctgctggggcccactttc 2382 	2383 cccgotttaagcagctgctccgctgaccttaaagacatcctgagcgagc	2443 caactccttcagcaacagcagcagcagtatccgaaggcagcagcagcagggagagcg 2502 	2503 agggaggctccgacttcctccaaggacaattacttcgggggacattcgacc 2562 	2563 atttctgacaacgccaaggagttgtgtaaggcagtgtccgtgtccatgggcctgggtgtg 2622 	a 2682	274 340	2743 ggttctctgctagacgacagcgcaggcaagagcactgaagatactgctgagtattccct 2802 	2803 ttcaagggaggttacaccaaagggctagaaggcgagagcctagtgctctggcagcgct 2862 	2863 gcagcaggagatccgggacattgaattgcgtctacctgtctctctacaagtccgga 2922
Qy	Qy Db	Oy Dp	Qy Db	Qy	Oy Dp	Qy	Oy Db	Oy Db	Oy Db	Qy Db	Oy Db	Qy Db	Qy Db	yo, da	Oy Db	Qy Db 3	Qy Db 3

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Specific region in hormone binding domain is essential for hormone binding and trans-activation by human androgen receptor Mol. Endocrinol. 4 (3), 417-427 (1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. 1 (bases 1 to 3231)
Govindan,M.V.
tecteatectggcacaeteteteacageegaagaaggeeagttgtatggaeegtgtggt 3222
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Human testis and prostate cancer cell line LNCaP, cDNA to mRNA.
Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HUMARX 3231 bp mRNA PRI
Human androgen-receptor mRNA, complete cds.
M34233
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109. .2829
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109. .2829
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ASAAPPGASILLLQQQQQQQQQQQQQETSPRQQQQQGEDGSPQAHRRGPTGYLV
LDEEQQPSQALECHPERGCVPEPGANVASKGLPQQLAPPDEDDSAAPSTELLL
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713 a 941 c 883 g 654 t

BASE COUNT 713 a 941 c 883 g 694 t ORIGIN

4; 2535 2415 2355 1875 1935 1995 2055 2175 2235 2295 agctagctgcagcgactaccgcatcaccagcctgttgaactcttctgagcaagagaag 1815 180 240 393 453 513 633 120 Gaps 9 aatctgttccagagcgtgcgcgaagtgatccagaacccgggccccaggcacccagaggcc aaggggctgccgcagcagctgccagcacctccggacgaggatgactcagctgccccatcc GACATCCTGAGCGAGGCCAGCACCATGCAACTCCTTCAGCAACAGCAGCAGGAAGCAGTA tccgaaggcagcagcagcgggagagcgagggaggcctcggggggctcccacttcctccaag agccccaggcagcagcagcagcagcaggtgaggatggttctccccaagcccatcgtaga gacatectgagegaggecageaceatgeaactectteageaacageageaggaageagta gggaggcggggtaagggaagtaggtggaagattcagccaagctcaaggatggaagtgcag AATCTGTTCCAGAGCGTCCGCGAAGTGATCCAGAACCCGGGCCCCAGGCCACCCAGAGGCC gcgagcgcagcactcccggcgccagtttgctgctgctgcagcagcagcagcagcagcag AAGGGGCTGCCGCAGCAGCTGCCAGCACCTCCGGACGAGGATGACTCAGCTGCCCCATCC 53; 3231; Length Indels 21; 6; GCGAGCGCACCTCCCGGCGCCCAGTTTGCTGCTGCT----DB Score 3089.4; Pred. No. 0; 0; Mismatches Query Match 60.8%; Best Local Similarity 97.7%; Matches 3195; Conservative 2296 2356 2416 1876 2056 2116 2176 2236 1756 ı 1816 61 121 1936 181 1996 241 279 334 394 454 634 g Óγ Q δy g δy qq qq δ Op οy q ò Dp QY ŏ g δy qq οy δ ò ò

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Specific region in hormone binding domain is essential for binding and trans-activation by human androgen receptor Mol. Endocrinol. 4 (3), 417-427 (1990) 90258935
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Query Ma Best Loo Matches	Qy 1816 Db 7	Qy 1876 Db 67	Qy 1936 Db 127	Oy 1996 Db 187	Qy 2056 Db 232	Oy 2116 Db 293	Qy 2176 Db 353	Oy 2236 Db 413	Oy 229 Db 47	Qy 235 Db 53	Qy 241	Oy 247 Db 65	Qy 253 Db 71	Qy 259 Db 77	Qy 265 Db 83	OY 271 Db 89	Qy 277 Db 95

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Marcelli, M., Tilley, W.D., Wilson, C.M., Griffin, J.E., Wilson, J.D. and McPhaul, M.J.

Befinition of the human androgen receptor gene structure permits the identification of mutations that cause androgen resistance: premature termination of the receptor protein at amino acid residue $88 causes complete androgen resistance mod. Endocrinol. 4 (8), 1105-1116 (1990)
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 3061)
Tilley,W.D., Marcelli,M., Wilson,J.D. and McPhaul,M.J.
Characterization and expression of a cDNA encoding the human
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Draft entry and computer-readable sequence [1] kindly submitted M.J. McPhaul. 09-Dg2-1988.

Location/Qualifiers
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PRI 16-SEP-1999 complete cds.

Pan troglodytes androgen receptor mRNA, U94177

LOCUS DEFINITION

ACCESSION

RESULT 10

PTU94177

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/ULTAINSTALL OIL SOOLAL/
// LTAINSTALL OIL SOOLAL/
// LTAINSTALL OIL SOOLAL/
// LTAINSTALL OON-"MENOGLGGROOQQQQQETSPRQQQQGEDGSPQAHRRGPT
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MGRRSFTNNNSRMLYFAPDLLIKSHWARRLDFRRHUNDDGAATUSSWWGLMVFA
MGRRSFTNNNSRMLYFAPDLLIKSHWARRLDFRTACKRRHSTSGSRRFYQLTFLLD
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Choong,C.S., Kemppainen,J.A. and Wilson,E.M.
Direct Submission
Submitted (18-MAR-1997) Laboratories for Reproductive Biology,
University of North Carolina at Chapel Hill, CB 7500, MSRB, Rm
UNC-CH, Chapel Hill, NC 27599, USA
Location/Qualifiers
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Choong, C.S., Kemppainen, J.A. and Wilson, E.M.
Evolution of the primate androgen receptor: a structural
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/protein_id="AAC73048.1"
/db_xref="G1:3861477"
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98404153
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/db_xref="taxon:9598"
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Db Qy	qq	da da	d Db	Oy Dp	A GG S	og co.	qa d	da o	op Op		Oy Dp	do oy	G 6	S Q	QY	QY Db	ορ	Qy Db
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	agteggeee 	gtggccgccagca 	ccccatccac	ctgaccttaaagacatcctgagcct	aggaagcagta 	cttcctccaag 	tgtgtaaggca 	cagggaacagcttcgggggg CGGGGAACAGCTTCGGGGGG	gtgegteeeact 	gcaggcaagagcactg	ggctagaaggc 	ttgaactgccg	cagagtege 	ccgcctccccat	GCCTCCCCAT 199c99ctgcc 	Aac SAC	94 – 94 1 – 94	662662662
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racggetacactcggececeteaggggetggegggecaggaaagegaette 3363

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AF162704 2827 bp mRNA PRI 29-JUL-1999
Homo sapiens cell-line MDA-MB-453 androgen receptor mRNA, complete
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Mammalia; Eutheria; Primates, Catarrhini; Hominidae; Homo.

    (bases 1 to 2827)

                                                                                                                                                                                                                                                                                                                                                                                                                carcinoma MDA-MB-453
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CA 92121
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San Diego,
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Jin,C.H., Urcan-Bisel,M.S. and Sch.
Direct Submission
Submitted (25-JUN-1999) Endocrine
Inc, 10255 Science Center Drive, S.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="MDA-MB-453"
                                                                                                                                                                                                                                                                                                                                                                                                   Jin, C.H., Urcan-Bisel, M.S. and Androgen receptor sequences in
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                                                                                                                                                                                                                             GI:5639998
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AF162704.1
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EMGPWNDSYSGPYGDMRLETARDHVLPIDYYFPPQKTCLICGDEASGCHYGALTCGSC
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ARELHQFTPDLLIKSHWYSVDFPEMMAELISVQVPKTLLSGKVKPIYFHTQ"

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                                                                                           54.1%; Score 2748; Diarity 98.1%; Pred. No. 0; Conservative 0; Mismatches
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Matches 2822;
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Best Local
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AAACTACAGGAGGAAGGAGGAGGGCTTCCAGCACCACCAGCCCCACTGAGGAGACA 1929
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179
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aca fascicularis
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Choong/C.S., Kemppainen,J.A. and Wilson,E.M.
Direct Submission
Submitted (18-MAR-1997) Laboratories for Reproductive Biology,
University of North Carolina at Chapel Hill, CB 7500, MSRB, Rm
UNC-CH, Chapel Hill, NC 27599, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          atggaagtgcagttagggctgggaagggtctaccctcggccgccgtccaagacctaccga 1923
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                     Cercopithecinae; Macaca.
1 (bases 1 to 2821)
Choong, C.S., Kemppainen, J.A. and Wilson, E.M.
Evolution of the primate androgen receptor: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 9;
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    1. .2821
    /organism="Macaca fascicularis"
/db_xref="taxon:9541"

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0; Mismatches
Eutheria; Primates;
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95.38;
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Matches 2771; Conservative
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J. Mol. Ev
98404153
9732460
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AUTHORS
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Choong, C.S., Kemppainen, J.A. and Wilson, E.M.
Choong, C.S., Kemppainen, J.A. and Wilson, E.M.
Direct Submission
Submitted (18 MAR-1997) Laboratories for Reproductive Biology,
University of North Carolina at Chapel Hill, CB 7500, MSRB, Rm 370,
UNC-CH, Chapel Hill, NC 27599, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                               Cercopithecinae; Papio.
1 (bases 1 to 2569)
Choong, C.S., Kemppainen, J.A. and Wilson, E.M.
Evolution of the primate androgen receptor: a structural basis for
                                                                                                                                                                                                                                                                                                                                                                        Bukaryota; Mėtazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                       2494 ITCIACCAGCICACCAAGCICCTGGACTCCGTGCAGTTTGCGAGAGAGAGCTGCATCAG 2553
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J. Mol. Evol. 47 (3), 334-342 (1998)
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2943 3003 3063 1143 3183 2883 1263 3243 3303 1356 3363 1416 3423 1476 3483 1536 3543 1596 3603 1656 963 3663 1716 3723 3783 1836 903 3903 1956 GCAGGCAAGAGCACTGAAGATACTGCTĠAGTATTCCCCTTTCAAGGGAGGTTACACACAAA taccagagtegegactactacaactttecactggetetggecggacegececeteeg atgogtttggagactgccagggaccatgttttgcccattgactattactttccacccag actigitatcaaaagcgaaaigggcccciggaiggaiagciaciccggacciiacggggac ctgaaactacaggaaggaaggagtttccagcaccaccagccccactgaggagacaacc 2944 2884 1024 1084 1144 2824 964 3004 3064 3124 1204 3184 1264 3244 1357 1306 3304 3364 1417 3424 1477 1537 1597 3484 3544 1657 3664 1717 1777 3604 3724 3784 1837 qq δ Q δλ Db οy qq Db QQ οy g Qγ QΥ Οý qq Ω QQ QΥ Db φ Db Οy QQ QV Dp O.Y D.D Ω QQ οχ Db ογ ΩD δ Db ΩY q

SOUFCE BASE COUNT ORIGIN	Query Matc Best Loca Matches 3	75	Db 1 A QY 818 9	878	11 93	966	1056	297	117	302	1295	Db 481 A Qy 1355 t	Db 517 - Oy 1413 a	1473	Db 618 -	673	QY 1593 t	DP 733 C	Qy 1653 t	Db 793 T
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                                                                                                                                                                                                                                                                                                                        Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Draft entry and computer readable sequence [1] kindly submitted E.M.Wilson, 18-AUG-1988.
                                                                                                                                                                                                                                                                                                                                                                                                                   The rat androgen receptor: Primary structure, autoregulation of messenger ribonucleic acid, and immunocytochemical localization
                                 gettgittacagcae--tactetgigecagecacacaaaacgittactiatettatgecae 5016
                                                  4016 GCTTGTTTATAGCACTGTGCTGTGCCAACCAAGCAAATGTTTACTCACCTTATGCCAT 4075
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GAGTITIGITGIATITCTTCAAGTCTGTGATGATCTTCTTGTGGCCCAGTGTCAA-CTGT 4015
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                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleost
Sciurognathi; Muridae; Murinae;
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Tan, J., Joseph, D.R., Quarmby, V.E., Lubahn, D.B., and Wilson, E.M.
                                                                                                                                                                                                   ROD cds.
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/db_xref="taxon:10116"
994. .3702
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Pred. No. 0;
0; Mismatches
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Mol. Endocrinol. 2, 1276-1285 (1988)
89112209
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                                                                                                                                                                                                                              (AR) mRNA,
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Rodentia;
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Rat, epididymal cDNA
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                         M20133.1 GI:202895
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